TABLE I

cDNA	Embryo Phase	Clone	Nucleotide Sequence
SEQ ID NO:332	Early	LPS-102	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAG GCGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCTC TCCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGG CTTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCA TCTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGAC TGACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTC AGTTAAGGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCC TCACAGCAAAAGATGCGTCGGAGCTCGTTGATTCTTTAGTTTGAACGGTCATACCT TTATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAATTTA GGTGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTT ATCTAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTA AAATTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGGGAGGAATTTATT GAAATCACAAGTTTGATGGGTAACCCATCCATATATACAGTAAAAAGATCAGTTTAA ATAACACAATACCACACAATAACGAAGAGTCCAAAAAATGCACTAAAAACAAGTCTT TTATTATATTGGCTTACATTTATTTTTTACTTTTATTCACTTGGATAGTAAAAGAGAAA TTAATTTTTAATATTTTATTATATCTATACTACATTAAATATTCTATATAATGTTAACTC TAAAAAACATTTAAGATTTATATATGGTCAATTACCCTTATATAATCTTTAACTTTAAA TCCCTGATGGGGGGCCAATAANGGTNGGGAAACTAACGGAAN
SEQ ID NO:333	Early	LPS-103	ACTATAGGGCACGCGTGGTCGACGGCCCGGGCTGGTTTCAATAAATTCCTCCCGG ATTTTAGAGAAATTAGACCATAAAAACTCACGAAAAAAATTTTAGACCATAAAAACTC ACGAAAAAAACTTCCCCAAAATCACGCTAAAAACAACTAGATAAAAAAATACCCATC TTTGATGATGTGGATAGTGACAGCCTATTCCAAACTATCACCTAAATTGTAAGTTAC ATGCATAACACGATGACCTCATCTATACGTTGTGCCAAATAAAGGTATGACCGTTCA AACTAAAGAATCAACGAGCTCCAACGCATCTTTTGCTGTGAGGATTCTCACGGCTA ACATTCATGACCGATTACCTCCTACCAACAAGGCTTTAACTGAACAATCCAAACAAT TACAGCTAACAATCAACGGGCGCCAACGGATCATTTTGTCAGCCTCGAAGCAGCAT TGTTATATGTATATGAATAGAATAGATCAATGTAACTTGGAGATGCTAATTTGAAGC CCTTCTCTGAAGGTGGACAATTCCAGCACCAGTGGTCTAAAGCCTCAATATGGCTA TAGAAATTCTTCTGGGGGGTTGCACCTATGGAAGAGGGTCGGAGAGGACGAAGCTG TGGATCGCTCTTACCATCT
SEQ ID NO:334	Early	LPS-104	ATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCTATGGTCGACCTGCAGG CGGCCGCGAATTCACTAGTGATTAGATGGTAAGAGCGATCCACAGCTTCGTCCTCT CCGACCCTCTTCCATAGGTGCAACCCCCAGAAGAATTTCTATAGCCATATTGAGGC TTTAGACCACTGGTGCTGGAATTGTCCACCTTCAGAGAAGGGCTTCAAATTAGCAT CTCCAAGTTACATTGATCTATTCTATTCATATACATATAACAATGCTGCTTCGAGACT GACAAAATGATCCGTTGGCGCTCGTTGATTGTTAGCTGTAATTGTTTGGATTGTTCA GTTAAGGCCTTGTTGGTAGGAGGTAATCGGTCATGAATGTTAGCCGTGAGAATCCT CACAGCAAAAGATGCGTTGGAGCTCGTTGACTCTTTAGTTTGAACGGTCATACCTT TATTTGGCACAACGTATAGATGAGGTCATCGTGTTATGCATGTAACTTACAGTTTAG GTGATAGTTTGGAATAGGCTGTCACTATCCACATCATCAAAGATGGGTATTTTTTTA TCTAGTTGTTTTTAGCGTGATTTTGGGGAAGTTTTTTTCGTGAGTTTTTATGGTCTAA AATTTTTTTCGTGAGTTTTTATGGTCTAATTTCTCTAAAATCCGAGAGGAATTTATTG AAACCAGCCCGGGCCGTCGACCACGCGTGCCCTATAGTAATCGAATTCCCGCGGC CGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGT CGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGCG TACCCACTTAATCGCCTTGGAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGA AGAGGCCCGGACCCGATCGGCCCTTTCCAACAAATTGCGCAACCCTGAATNGGGA AATGGGCCCCCCCCTNTTACCGGNGCAATTAAACCCCGGGGGGGNGNGGGGGTT CCCCCCCCCGTGGACCT

TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPS001	0	249.4	1400.9	827.6	1683.8	2019.4	189.2	4303.9
LPS003	701.2	555.9	2815.2	2445.1	3249.9	3094.7	227.1	3111.6
LPS004	466.1	335.5	2652	2701	2644	2329.6	218.5	2332.4
LPS006	753.1	332.7	3287.3	2964.5	2832.2	2688.9	182.1	1591.9
LPS007	685.2	226	2010.2	1911.3	2600.4	1730.1	181.5	2737.7
LPS008	652.8	274.8	2415	2219.3	2607.1	2294.9	155.7	1292.1
LPS010	558.3	356.1	2667.6	2881.1	2584.3	1573.4	161.7	1041
LPS011	3536.1	424.7	4021.5	3793.8	3590	3182	160.5	1471.7
LPS012	809	408.4	2206.7	2187.1	2282.2	2422.5	462.4	1483.2
LPS013	1211.1	391.6	2294.7	2652.6	2005.4	2167.8	166.8	1570.5
LPS014	2191.9	432.5	2651.8	3013.5	3341.2	3586.7	178.8	3527.1
LPS015	1197.9	306	5651.4	14828.6	20242.8	21558.2	1427.2	34472.3
LPS019	1830.2	334.5	3329	3954.4	4347.5	4658.2	312.1	4743.1
LPS020	675.2	327.8	2258.3	2284.7	2542.7	2321.4	171.9	1609.8
LPS023	451.3	337.5	1401.9	1106.8	1766.2	1842.6	109.6	1365.2
LPS024	4585.8	444.5	3006.3	3431.1	3548.8	3759	157.3	4062.3
LPS025	5102.3	397.1	4322.9	4699.6	5067	4973.2	262.4	5240.4
LPS026	1568.7	285.9	1809.9	1830.4	2829.9	2381.7	164.9	1404.9
LPS027	5499.9	458.4	4853.9	5218.6	2598.4	1756.6	457.9	2375.3
LPS028	4812.9	314.9	2368.8	2616.5	3113.3	3292.4	557	4146
LPS029	4464.6	251.2	2334.4	2058.1	2930.3	3219.3	472	3814.4
LPS030	1142.2	352.5	2519.8	2460.9	2499.8	2634.5	378.3	2147.8
LPS031	1067.7	481.6	3510.8	2799.2	3568.2	3257.2	287.9	2209.7
LPS032	1120.2	332.3	3153.1	3032.4	1769.2	1816.7	146.6	2689.9
LPS036	1498.2	1072.9	4633.6	5524.2	5465.1	6350.7	918	14058.5
LPS037	1890.3	320.9	3719.1	3618.9	4138	4518.1	513.4	5087.5
LPS038	2899.5	310.3	4530	4226.1	4491.6	3969	268.4	4245.3
LPS040	527.4	238.1	1433.4	1611.2	1984.5	1506.5	143.9	1988.7
LPS041	506.1	265.5	1958.9	2843.2	2065.3	2016.2	147.4	2781.7
LPS042	1432.1	1140.3	4379	4973.3	4525.4	4340.8	319.6	3009.8
LPS043	696.9	776.2	3933.1	4894.3	3512.2	3664.7	340.6	3098.4
LPS044	57.8	275.1	3365	4261.2	4773.5	4979.9	974.4	10645.5
LPS045	536.1	211.1	1559.5	1415	1498.5	1584.8	562.1	1912.3
LPS046	796.3	231.7	1023.9	306.4	1417.8	1328.2	83.8	946.4
LPS047	5029.9	518.2	3632.5	4262.1	4755.5	4087.9	386.3	4933.8
LPS050	6333.5	2620.8	5271.4	5242.1	5586.4	5560.1	980.1	11444
LPS051	1378	224.4	2328.8	2221.8	2260.5	2715.1	123.7	3670.4
LPS052	1526.4	267.5	2046	1856.2	2186.5	2416.3	99.3	2010.1
LPS053	4438.3	361.6	4087.6	3959.9	4786.5	3666.8	379.6	4256.7
LPS054	1992.9	269.9	2734.2	2388.1	3143.8	2337.7	177.6	2803.9
LPS055	4587.8	334.4	3488.6	3474	4018.3	3101.6	196.2	4309.4
LPS056	5960.7	1333.7	5338.8	5670.3	5674.4	5533.5	446.4	5593
LPS057	2219.9	301.9	2397.3	2356.1	2218.1	2085.6	184.4	2657.8
LPS058	4070.4	299.9	3485.4	3721.3	4113.8	4142.2	239.8	4945.6
LPS059	8729.3	279.2	3885.7	3636	2720.4	3346.7	165.7	3734
LPS060	4580.2	323.7	3027.8	4713.4	4929.1	5047.5	161	4704.8
LPS061	2831.9	366.8	2392	2327.7	2546.5	1991.8	177.9	3036.7
LPS062	1674.1	353	2711.2	2526.1	1847	1830.3	124.5	3584.2
LPS063	5514.4	419.8	5238.9	5020.3	5417.4	5041	250.1	4812.6
LPS064	7417	3166	5229.5	7497.4	7933.1	10261	1088.3	16829.6

TABLE II

Clone	SE1-SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9
LPS065	5634.9	343.5	5527.8	5099.4	7833.4	5356.6	237.5	4696.7
LPS066	1015.9	244.5	1702.6	1650.5	2895.1	2437.2	128	2514.1
LPS067	2796.8	240.4	3931.5	4810.3	5407.8	5418.3	202.5	9403.8
LPS069	533.4	189.9	1635.8	1816.4	2114.2	1646.8	119.8	3208.8
LPS070	2516.9	240.6	1909.5	2519.6	2156.7	1777.4	186.4	4362.1
LPS071	592.8	196.4	1789.2	2189.2	1981.1	1304.5	127.6	3430
LPS072	444.2	217.6	1422.9	1509	2065.3	2289.9	122.7	2678.8
LPS073	4362.8	273.1	3094.9	3348.1	3771.8	4075.3	137.7	4259.6
LPS074	32072.9	6816.3	33531	25258.9	38176.4	32687.7	14607.1	37529.6
LPS075	7013.9	472.7	4759.7	4933.9	5452.2	5408.7	409.4	5397.1
LPS076	4236.1	362.6	3131.9	2882	3368.5	3354.6	119.5	3141.9
LPS077	2958.7	276.6	4380.4	4862.5	4475.1	4958.7	218.9	4426
LPS078	23685.3	2642.5	35458.6	25869.6	42378.9	33047.1	25402.2	37189.8
LPS079	4794.3	547.8	4628.6	4821.8	5257.2	5277	829.5	5449.7
LPS080	30454	10527	33713.7	23785.4	32590.9	32210.7	16224.4	37659.2
LPS081	30405.9	28677	35358.3	25873	22338.1	31715.3	36436.4	36650.5
LPS083	5040.1	460.8	3251.7	3487.3	2688.9	2565.9	190.5	2979.7
LPS084	2031	298.9	2843.7	2718.4	2352.2	2165.5	164.9	3398
LPS086	3571.7	320.1	2715.8	2648	1989	2528.4	143.9	2969.7
LPS087	3302.3	337.4	4873.1	5695.8	5407.2	5450.6	670.8	18404.9
LPS088	826.8	302.1	2389.2	2871.1	3180.8	2635.2	138.6	3141.5
LPS089	796.4	321.2	1987.7	2640.6	3299.1	2285.1	143.7	3176.6
LPS090	4031	235.9	3867.3	4064.4	4503.3	4798.4	341.7	4697.7
LPS091	2423.3	196.5	2836.8	3101.3	4049.1	4172	295.2	4612.2
LPS092	2914.9	208.5	4005.3	3138.4	3911.6	4036.1	270.4	4842.9
LPS093	793	195.5	1619.2	1331.6	1909.3	1843	147.1	2772
LPS094	1374	221	2205.5	2028.5	2240.9	2632.2	163.3	2849.1
LPS095	728.7	174.1	2022.6	2112.1	2335.8	1264.6	117.5	2957
LPS096	393.3	168.5	1531.9	1393.4	1893.3	869.1	118.3	1691.1
LPZ001	2008.6	185.4	2535.9	2937.9	3472	1981.8	118.9	2421.7
LPZ002	3529.3	384.6	4579.3	4474.6	3236.7	3855.8	313.8	3237.5
LPZ003	4076.8	275.4	2651.2	2966.7	2829.2	4177.4	378.5	4369.7
LPZ004	5595	687.4	5468.2	5615.9	5243.6	5699.6	601.6	5889.9
LPZ005	5680.5	3353	34994.7	26121.9	42555.1	33144.5	16193.7	37798.2
LPZ006	1199.8	299.4	3013.7	3099.8	3517.3	3397.1	140.6	3370.8
LPZ007	1159.1	462.2	3292.7	2992.5	3121.4	2936.7	235.5	3238.6
LPZ008	1874.3	237.7	3110.8	3236.7	2516.5	3182.2	325.3	4330.1
LPZ009	3331.1	296.3	2348.5	3414	2478.2	3309.5	348	5658.1
LPZ010	3216.3	1186.8	4977.3	5024.7	4564.4	4992.4	442.6	4454.5
LPZ011	4613.4	910.9	4510.7	4515.7	3729	4357.3	371.4	4695.9
LPZ012	1531.5	469.5	2915.3	2611.1	2012.3	3481.4	270.3	3804.3
LPZ013	3495.1	268.8	2125.9	2584.7	3194.7	3787.4	125.1	4929.6
LPZ015	2040	257.6	1971.1	2966.7	2191.1	3056.7	227.1	4156.6
LPZ016	5307	2761.1	8451.7	17219.7	22792.7	15567.3	1073.6	35074.1
LPZ017	2476.4	354.3	3175.5	4330.8	4496.2	4061	273.2	5328.9
LPZ018	3929.4	417.5	12420.2	14916.1	18116	17637.5	2541.6	31981
LPZ019	5404.2	427.3	32190.3	24710.4	42102.7	32342.6	19528	36969.5
LPZ020	576.9	142.9	1451.4	1505.4	3534.8	2679.8	210.9	3046.2
LPZ022	1408.2	155.2	2406.7	2845.7	3042.5	3074.8	189.9	3829.2
LPZ023	562.1	152.8	2096.7	1710	2045.5	2078.9	200.8	2874.3